

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 30, 2002, 11:50:30 ; Search time 27.34 Seconds
(without alignments)
39.007 Million cell updates/sec

Title: US-09-432-546-5
Perfect score: 103
Sequence: 1 SRPMPWMPKWPMLI 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|------------------------|
| 1 | 62 | 60.2 | 144 | 1 JCI222 | indolicidin precursor |
| 2 | 57 | 55.3 | 1662 | 2 T18540 | mofa protein precursor |
| 3 | 56 | 54.4 | 236 | 2 U00606 | arylesterase (EC 3 |
| 4 | 56 | 54.4 | 236 | 2 F83705 | hypothetical prote |
| 5 | 53.5 | 51.9 | 497 | 1 A40487 | ferredoxin--NADP+ |
| 6 | 53 | 51.5 | 95 | 2 E86447 | protein FSD14.5 [1 |
| 7 | 52.5 | 51.0 | 970 | 2 C84488 | hypothetical prote |
| 8 | 52.5 | 51.0 | 1231 | 2 C84716 | hypothetical prote |
| 9 | 52 | 50.5 | 301 | 2 G83556 | hypothetical prote |
| 10 | 52 | 50.5 | 1112 | 2 S70522 | cyclic nucleotide |
| 11 | 51.5 | 50.0 | 196 | 2 B48232 | cysteine-rich exte |
| 12 | 51.5 | 50.0 | 209 | 2 A48232 | photosynthetic rea |
| 13 | 51.5 | 50.0 | 279 | 2 S68239 | photosynthetic rea |
| 14 | 51.5 | 50.0 | 279 | 2 E49664 | photosynthetic rea |
| 15 | 51.5 | 50.0 | 279 | 2 T50889 | photosynthetic rea |
| 16 | 51.5 | 50.0 | 321 | 2 F84611 | hypothetical prote |
| 17 | 51.5 | 50.0 | 498 | 1 J70751 | ferredoxin--NADP+ |
| 18 | 51.5 | 50.0 | 2970 | 2 T08839 | polyprotein - marm |
| 19 | 51 | 49.5 | 1173 | 1 VGIHHC | E2 glycoprotein pr |
| 20 | 50.5 | 49.0 | 560 | 2 T32661 | hypothetical prote |
| 21 | 50 | 48.5 | 83 | 2 B72392 | hypothetical prote |
| 22 | 49.5 | 48.1 | 253 | 2 G70715 | hypothetical prote |
| 23 | 49.5 | 48.1 | 257 | 2 S70177 | hypothetical prote |
| 24 | 49 | 47.6 | 169 | 2 F72532 | hypothetical prote |
| 25 | 49 | 47.6 | 456 | 1 I40516 | spaf protein - Bac |
| 26 | 49 | 47.6 | 669 | 2 T28028 | hypothetical prote |
| 27 | 48.5 | 47.1 | 212 | 2 S57330 | cathelein-like anti |
| 28 | 48.5 | 47.1 | 228 | 2 S40463 | prophenin (PF-2) p |
| 29 | 48 | 46.6 | 314 | 2 H84677 | hypothetical prote |

| | | | | | |
|----|------|------|------|----------|--------------------|
| 30 | 48 | 46.6 | 947 | 2 H85088 | hypothetical prote |
| 31 | 48 | 46.6 | 990 | 1 G46335 | env polyprotein pr |
| 32 | 48 | 46.6 | 1172 | 2 F96503 | protein F9C16.13 l |
| 33 | 47.5 | 46.1 | 111 | 2 T29295 | hypothetical prote |
| 34 | 47.5 | 46.1 | 248 | 2 S23449 | NADH oxidase (H202 |
| 35 | 47.5 | 46.1 | 752 | 2 E82146 | Rec2-related prote |
| 36 | 47 | 45.6 | 73 | 2 D75497 | hypothetical prote |
| 37 | 47 | 45.6 | 212 | 2 PQ0518 | envelope protein - |
| 38 | 47 | 45.6 | 233 | 2 B96552 | protein F23N19.5 l |
| 39 | 47 | 45.6 | 253 | 2 D86310 | protein F113.4 l[m |
| 40 | 47 | 45.6 | 299 | 2 T12505 | hypothetical prote |
| 41 | 47 | 45.6 | 964 | 1 VCLJ06 | env polyprotein pr |
| 42 | 47 | 45.6 | 966 | 1 VCLJ06 | env polyprotein pr |
| 43 | 47 | 45.6 | 982 | 1 VCLJVS | env polyprotein pr |
| 44 | 47 | 45.6 | 983 | 1 E45390 | env polyprotein pr |
| 45 | 47 | 45.6 | 1055 | 2 A96682 | protein F1E22.12 l |

ALIGNMENTS

RESULT 1
JCI222
Indolicidin precursor - bovine
N:Alternate names: antimicrobial peptide
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JCI222; A42387; S25664
R:del Sal, G.; Storici, P.; Schneider, C.; Romeo, D.; Zanetti, M.
Biochem. Biophys. Res. Commun. 187, 467-472, 1992
A>Title: cDNA cloning of the neutrophil bactericidal peptide indolicidin.
A:Reference number: JCI222; MUID:92392368
A:Accession: JCI222
A:Molecule type: mRNA
A:Residues: 1-144 <SAL>
A:Cross-references: EMBL:X67340; NID:9462; PIDN:CAA47755.1; PID:9463
A:Experimental source: bone marrow
J:Seasted, M.E.; Novotny, M.J.; Morris, W.L.; Tang, Y.Q.; Smith, W.; Cullor, J.S.
J. Biol. Chem. 267, 4292-4295, 1992
A>Title: Indolicidin, a novel bactericidal tridecapeptide amide from neutrophils.
A:Reference number: A42387; MUID:92165771
A:Accession: A42387
A:Molecule type: protein
A:Residues: 131-143 <SEL>
A:Experimental source: neutrophils
A>Note: sequence extracted from NCBI backbone (NCBI:83840)
C:Superfamily: cathelein; cystatin homology
C:Keywords: amidated carboxyl end
F:1-29/Domain: signal sequence #status predicted <SIG>
F:22-129/Domain: cystatin homology <CVS>
F:30-130/Domain: propeptide #status predicted <PRO>
F:131-143/Product: indolicidin #status experimental <MAT>
F:143/Modified site: amidated carboxyl end (Arg) (amide in mature form from following

Query Match 60.2% Score 62; DB 1; Length 144;
Best Local Similarity 75.0% Pred. No. 0.24;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RMPMPWK 10
DB 135 KMPMPWR 142

RESULT 2
T18540
mofa protein precursor [imported] - Leptothrix discophora
C:Species: Leptothrix discophora
C>Date: 02-Sep-2000 #sequence revision 02-Sep-2000 #text_change 08-Sep-2000
C:Accession: T18540
R:Corstjens, P.L.
submitted to the EMBL Data Library, April 1999
A:Reference number: Z18959

A:Accession: T18540
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1662 <COR>
 A:Cross-references: EMBL:225774; NID:e1427784; PID:e267517; PIDN:CAA81037.1
 C:Genetics:
 A:Note: mofa
 F:1-33/Domains: signal sequence #status predicted <SIG>
 F:43-1662/Product: mofa protein #status predicted <MAT>

Query Match 55.3%; Score 57; DB 2; Length 1662;
 Best Local Similarity 63.6%; Pred. No. 10;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 RMPMPMPKMP 13
 DB 490 RMHMGFMPV 500

RESULT 3

J00606
 Arylesterase (EC 3.1.1.2) precursor - Pseudomonas fluorescens
 C:Species: Pseudomonas fluorescens
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Mar-2000
 C:Accession: J00606
 R:Choi, K.D.; Jeon, G.H.; Rhee, J.S.; Yoo, O.J.
 Agric. Biol. Chem. 54, 2039-2045, 1990
 A:Title: Cloning and nucleotide sequence of an esterase gene from Pseudomonas fluorescens
 A:Reference number: J00606; MUID:91182405
 A:Accession type: J00606
 A:Residues: 1-236 <CHO>
 A:Cross-references: GB:D12484; GB:D01134; NID:g216856; PIDN:BA02052.1; PID:dl002534; PI
 A:Note: part of this sequence, including the amino end of the mature protein, was confir
 C:Keywords: carboxylic ester hydrolase
 F:2-236/Product: arylesterase #status predicted <MAT>

Query Match 54.4%; Score 56; DB 2; Length 236;
 Best Local Similarity 42.1%; Pred. No. 2.1;
 Matches 8; Conservative 3; Mismatches 2; Indels 6; Gaps 1;

OY 1 SRRW-----PMWPKMPL 13
 DB 204 ARTWPRSTYPMWPKMRL 222

RESULT 4

F83705
 Hypothetical protein BH0446 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
 C:Accession: F83705
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: AB3650; MUID:20263314
 A:Accession: F83705
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-236 <STO>
 A:Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BA04165.1; GSPDB:GN00
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH0446

Query Match 54.4%; Score 56; DB 2; Length 236;
 Best Local Similarity 77.8%; Pred. No. 2.1;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 WMPKMPPLI 14

DB 192 WLPKMPPL 200

RESULT 5

A40487
 Ferredoxin--NADP+ reductase (EC 1.18.1.2), long form, precursor - human
 N:Alternate names: adrenodoxin reductase
 C:Species: Homo sapiens (hmn)
 C:Date: 24-Jan-1992 #sequence_revision 18-Oct-1996 #text_change 11-Jun-1999
 C:Accession: A40487; B40487; A36482
 R:Solish, S.B.; Picado-Leonard, D.; Morel, Y.; Kuhn, R.W.; Mohandas, T.K.; Hanukoglu,
 Proc. Natl. Acad. Sci. U.S.A. 85, 7104-7108, 1988
 A:Title: Human adrenodoxin reductase: two mRNAs encoded by a single gene on chromosome
 A:Reference number: A40487; MUID:89017146
 A:Accession: A40487

A:Molecule type: mRNA
 A:Residues: 1-497 <SOL>

A:Cross-references: GB:003826; NID:g178212; PIDN:AAB59498.1; PID:g178214
 A:Accession: B40487

A:Molecule type: mRNA
 A:Residues: 66-122, 'R', 124-203, 210-497 <SO2>

A:Cross-references: GB:003826
 R:Lin, D.; Shi, Y.; Miller, W.L.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8516-8520, 1990

A:Title: Cloning and sequence of the human adrenodoxin reductase gene.
 A:Reference number: A36482; MUID:91046028

A:Accession: A36482

A:Molecule type: DNA
 A:Residues: 1-122, 'R', 124-497 <LIN>

A:Cross-references: GB:M38255; GB:M58509; GB:M38256; NID:g178206; PIDN:AAA5166.1; PI
 C:Comment: Ferredoxin--NADP+ reductase is localized in the matrix of adrenal cortex m
 ferredoxin--NADP+ reductase, adrenodoxin and two forms of cytochrome P-450.

C:Genetics:

A:Gene: GDB:FMXR; ADXR
 A:Cross-references: GDB:119659; OMIM:103270

A:Map position: 17q24-17q25
 C:Function:

A:Description: catalyzes the reversible reduction of NADP+ by reduced ferredoxin or r
 C:Superfamily: human ferredoxin--NADP+ reductase

C:Keywords: alternative splicing; electron transfer; flavoprotein; mitochondrion; mon
 F:1-32/Domains: transit peptide (mitochondrion) #status predicted <SIG>

F:33-497/Product: ferredoxin--NADP+ reductase, long form #status predicted <MAT>
 F:33-203, 210-497/Product: ferredoxin--NADP+ reductase, short form #status predicted <
 F:40-69/Region: beta-alpha-beta FAD nucleotide-binding fold

F:179-189/Region: NADP binding #status predicted
 F:280/Binding site: substrate (Lys) #status predicted

Query Match 51.9%; Score 53.5; DB 1; Length 497;
 Best Local Similarity 61.5%; Pred. No. 8.8;
 Matches 8; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY 1 SRRWMPMPK-WP 12
 DB 3 SRCWRMGMSAMP 15

RESULT 6

E86447
 Protein FSD14.5 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: E86447
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Comn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Hultzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marzia
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: E86447
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-95 <STO>
A:Cross-references: GB:AE005172; NID:g8920603; PIDN:AAF81325.1; GSPDB:GN00141
C:Genetics:
A:Gene: F5D14.5
A:Map position: 1

Query Match 51.5%; Score 53; DB 2; Length 95;
Best Local Similarity 29.6%; Pred. No. 2.1;
Matches 8; Conservative 2; Mismatches 3; Indels 14; Gaps 1;

OY 2 RRPMPMP-----WKMPPL 14
||| |||
DB 59 RNMWMPVLVITDVGEWMSWMMWMPVL 85

RESULT 7
C84488
Hypothetical protein At2g07730 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: C84488
R:Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Molloy, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: C84488
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-970 <STO>
A:Cross-references: GB:AE002093; NID:g3327392; PIDN:AAC26674.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g07730
A:Map position: 2

Query Match 51.0%; Score 52.5; DB 2; Length 970;
Best Local Similarity 46.7%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

OY 4 WP-----WMPKW 11
||| |||
DB 739 WPTLFSGIWMWANKW 753

RESULT 8
C84716
Hypothetical protein At2g31080 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: C84716
R:Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Molloy, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: C84716
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1231 <STO>
A:Cross-references: GB:AE002093; NID:g3746069; PIDN:AAC63844.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g31080
A:Map position: 2

Query Match 51.0%; Score 52.5; DB 2; Length 1231;
Best Local Similarity 46.7%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

OY 4 WP-----WMPKW 11
||| |||
DB 1000 WPTLFSGIWMWANKW 1014

RESULT 9
G83556
Hypothetical protein PA0702 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83556
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A:Reference number: A82950; MUID:20437337
A:Accession: G83556
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <STO>
A:Cross-references: GB:AE004506; GB:AE004091; NID:g9946584; PIDN:AAG04091.1; GSPDB:GN00139
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0702

Query Match 50.5%; Score 52; DB 2; Length 301;
Best Local Similarity 70.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 WPMWPMKPL 13
||| |||
DB 97 WPMWPMKPL 106

RESULT 10
S70522
cyclic nucleotide phosphodiesterase, cGMP-inhibited (EC 3.1.4.-) - human
C:Species: Homo sapiens (man)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 19-May-2000
C:Accession: S70522
R:Murata, T.; Taira, M.; Manganello, V.C. FEBS Lett. 390, 29-33, 1996
A>Title: Differential expression of cGMP-inhibited cyclic nucleotide phosphodiesterases in human and rat.
A:Reference number: S70522; MUID:96314543
A:Accession: S70522
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-1112 <MUR>
A:Cross-references: EMBL:U38178; NID:g1145301; PIDN:AAC50724.1; PID:g1145302
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, January 1996
C:Keywords: phosphoric diester hydrolase
F:736-1006/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 50.5%; Score 52; DB 2; Length 1112;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 WPMWPMK 11
||| |||
DB 169 WPMWPMK 176

RESULT 11
B48232

cysteine-rich extensin-like protein 2 precursor - common tobacco
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
 C:Accession: B48232; PQ0474; S24616
 R:Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
 Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
 A:Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain
 A:Reference number: A48232; MUID:93342083
 A:Accession: B48232
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-196 <WUA>
 A:Cross-references: GB:L13440; NID:g310924; PIDN:AAA34060.1; PID:g310925
 R:de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
 Plant Cell 4, 1041-1051, 1992
 A:Title: Developmental expression of tobacco pistil-specific genes encoding novel extensin
 A:Reference number: PQ0474; MUID:93005740
 A:Accession: PQ0474
 A:Molecule type: mRNA
 A:Residues: 'MAG', 1-105 <GOL>
 A:Cross-references: EMBL:Z14014
 A:Experimental source: stigma, style; strain Petit Havana SRL
 C:Genetics:
 A:Gene: CELP-2
 C:Superfamily: glutelin
 C:Keywords: cell wall; extracellular matrix; fertilization
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-196/Product: cysteine-rich extensin-like protein 2 #status experimental <MAT>

Query Match 50.0%; Score 51.5; DB 2; Length 196;
 Best Local Similarity 43.8%; Pred. No. 6.3;

Matches 7; Conservative 1; Mismatches 1; Indels 7; Gaps 1;

QY 4 WPM-----WPMKP 12
 ||| ||: ||
 DB 40 WPMWPCYLTWPFPM 55

RESULT 12

cysteine-rich extensin-like protein 1 precursor - common tobacco
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
 C:Accession: A48233; PQ0475; S24617
 R:Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
 Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
 A:Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain
 A:Reference number: A48233; MUID:93342083
 A:Accession: A48233
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-209 <WUA>
 A:Cross-references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
 R:de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
 Plant Cell 4, 1041-1051, 1992
 A:Title: Developmental expression of tobacco pistil-specific genes encoding novel extensin
 A:Reference number: PQ0474; MUID:93005740
 A:Accession: PQ0475
 A:Molecule type: mRNA
 A:Residues: 39-209 <GOL>
 A:Cross-references: EMBL:Z14020; NID:g19918; PID:g19919
 A:Experimental source: stigma, style; strain Petit Havana SRL
 C:Superfamily: glutelin
 C:Keywords: cell wall; extracellular matrix; fertilization; glycoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-209/Product: cysteine-rich extensin-like protein 1 #status experimental <MAT>
 F:146/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 50.0%; Score 51.5; DB 2; Length 209;
 Best Local Similarity 43.8%; Pred. No. 6.7;
 Matches 7; Conservative 1; Mismatches 1; Indels 7; Gaps 1;

QY 4 WPM-----WPMKP 12
 ||| ||: ||
 DB 45 WPMWPCYLTWPFPM 60

RESULT 13

photosynthetic reaction center chain L, terbutryn-resistant - Rubrivivax gelatinosus
 C:Species: Rubrivivax gelatinosus
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
 C:Accession: S68239
 R:Ouchane, S.; Picard, M.; Astier, C.
 FEBS Lett. 374, 130-134, 1995
 A:Title: A new mutation in the pufL gene responsible for the terbutryn resistance phe
 A:Reference number: S68239; MUID:96049571
 A:Accession: S68239
 A:Molecule type: DNA
 A:Residues: 1-279 <OUC>
 A:Cross-references: EMBL:U30310; NID:g927301; PIDN:AAA73927.1; PID:g927302
 A:Experimental source: strain 1
 C:Genetics:
 A:Gene: pufL
 C:Superfamily: reaction center protein
 C:Keywords: photosynthesis; transmembrane protein

Query Match 50.0%; Score 51.5; DB 2; Length 279;
 Best Local Similarity 40.9%; Pred. No. 8.9;

Matches 9; Conservative 2; Mismatches 2; Indels 9; Gaps 2;

QY 1 SRRWP-WMPW-----KWPL 13
 :||| ||: ||
 DB 257 TRGWPWWGWWLNLPIWSQWPL 278

RESULT 14

photosynthetic reaction center complex L subunit, PufL - Rhodocyclus gelatinosus
 C:Species: Rhodocyclus gelatinosus
 C:Date: 06-Oct-1994 #sequence_revision 19-Jul-1996 #text_change 16-Feb-1997
 C:Accession: E49964
 R:Nagashima, K.V.; Matsura, K.; Ohyama, S.; Shimada, K.
 J. Biol. Chem. 269, 2477-2484, 1994
 A:Title: Primary structure and transcription of genes encoding B870 and photosynthetic
 A:Reference number: A49964; MUID:94132007
 A:Accession: E49964
 A:Molecule type: DNA
 A:Status: preliminary
 A:Residues: 1-279 <NAG>
 A:Note: sequence extracted from NCBI backbone (NCBIN:143423, NCBIPI:143428)
 A:Superfamily: reaction center protein

Query Match 50.0%; Score 51.5; DB 2; Length 279;
 Best Local Similarity 40.9%; Pred. No. 8.9;

Matches 9; Conservative 2; Mismatches 2; Indels 9; Gaps 2;

QY 1 SRRWP-WMPW-----KWPL 13
 :||| ||: ||
 DB 257 TRGWPWWGWWLNLPIWSQWPL 278

RESULT 15

photosynthetic reaction center complex chain L [imported] - Rubrivivax gelatinosus
 C:Species: Rubrivivax gelatinosus
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
 C:Accession: T50889
 R:Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsura, K.; Shimada, K.
 Submitted to the EMBL Data Library, November 1999
 A:Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photos

A:Reference number: Z25270
A:Accession: T50889
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-279 <NAG>
A:Cross-references: EMBL:AB034704; PIDN:BAA94042.1
A:Experimental source: strain IL144
C:Genetics:
A:Gene: pufl
C:Superfamily: reaction center protein

Query Match 50.0%; Score 51.5; DB 2; Length 279;
Best local similarity 40.9%; Pred. No. 8.9;
Matches 9; Conservative 2; Mismatches 2; Indels 9; Gaps 2;
QY 1 SRRWP-WMPW-----KWPL 13
: 1 1 1 1 1 : 1 1 1
Db 257 TRGWPEWGMGWLNLPIWSOWPL 278

Search completed: January 30, 2002, 11:50:30
Job time: 124 sec

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2